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SEQUENCE LISTING

APR 1 7 2002

```
<110> Von Schaewen, Antje
          <120> Plant GntI Sequences and the Use Thereof for the Production ECH CENTER 1600/2900
                 of Plants Having Reduced or Lacking N-acetyl Glucosaminyl
                 Transferase I(GnTI) Activity
           <130> 032266-003
           <140> US 09/591,466
           <141> 2000-06-09
           <150> EP 98/08001
            <151> 1998-09-12
 APR 1 5 2002 2 160> 14
FADEWARK (210> 1
           <211> 1669
           <212> DNA
           <213> Solanum tuberosum
            <220>
            <221> misc feature
            <222> (659)...(667)
           <223> function: Asn codon in this context is a potential
                  glycosylation site;
                  product: N-glycosylation consensus sequence;
                  phenotype: N-glycans modulate protein properties;
                  standard name: N-glycosylatoin site;
                  label: pot-CHO;
                  note: GnTI-coding sequences from animals do not
                  contain this feature.
            <221> CDS
            <222> (53)...(1393)
            <223> codon_start: 53;
                  function: initiates complex N-glycans on secretory
                  glycoproteins;
                  EC number: 2.4.1.101;
                  product: beta-1,2-N-acetylglucosaminyltransferase I;
                  evidence: EXPERIMENTAL;
                  gene: cgl;
                   standard name: gntI;
                   label: ORF;
                  note: first gntI sequence from potato
                   (unpublished).
             <221> 5'UTR
             <222> (15)...(52)
             <221> 3'UTR
```

<222> (1394)...(1655)

| <221> <222> <223> | (80) fund production star production notes | ction duct: ndare | n: me : hyd d_nam ; dent: | embra droph me: n | nembi | ancho c ami cane comp | anch | or (| of a | type | e II | Golg | • | | | |
|---|--|-------------------------|---------------------------------------|-------------------------|------------------|--------------------------------|----------------------------|------------------|------------------|-------------------|-------------------|----------------------|------------------|-----------------------|-------------------|-----|
| <pre><221> misc_feature <222> (1)(14) <223> function: used for cloning the cDNA library in</pre> | | | | | | | | | | | | | | | | |
| <pre><221> misc_feature <222> (1656)(1669) <223> product: EcoRI/NotI-cDNA adapter; number: 2. <400> 1 gaattegegg cegeetgaga aaccetegaa tteaattteg catttggeag ag atg aga 58</pre> | | | | | | | | | | | | | | | | |
| <4002 gaatt | > 1 tege | gg co | cgcct | tgaga | a aad | ccctc | :gaa | ttca | aatt1 | tcg (| cattt | ggca | ıg aç | g atg Met 1 | aga Arg | 58 |
| ggg (| aac Asn | aag Lys 5 | ttt Phe | tgc Cys | ttt (Phe | gat t Asp I | ta d Leu <i>l</i> 10 | cgg Arg | tac Tyr | ctt (Leu : | ctc (Leu ' | gtc q Val V 15 | gtg (/al / | gct g Ala <i>F</i> | gct Ala | 106 |
| ctc Leu | gcc Ala 20 | ttc Phe | atc Ile | tac Tyr | ata Ile | cag a Gln 1 25 | atg Met | cgg Arg | ctt Leu | ttc Phe | gcg Ala 30 | aca Thr | cag Gln | tca (Ser (| gaa Glu | 154 |
| tat Tyr 35 | | gac Asp | cgc Arg | ctt Leu | gct Ala 40 | gct Ala | gca Ala | att Ile | gaa Glu | gca Ala 45 | gaa Glu | aat Asn | cat His | tgt (Cys ' | aca Thr 50 | 202 |
| | cag Gln | acc Thr | aga Arg | ttg Leu 55 | ctt Leu | att Ile | gac Asp | aag Lys | att Ile 60 | agc Ser | cag Gln | cag Gln | caa Gln | gga Gly 65 | aga Arg | 250 |
| gta Val | gta Val | gct Ala | ctt Leu 70 | gaa Glu | gaa Glu | caa Gln | atg Met | aag Lys 75 | cat His | cag Gln | gac Asp | cag Gln | gag Glu 80 | tgc Cys | cgg Arg | 298 |
| caa Gln | tta Leu | agg Arg 85 | Ala | ctt Leu | gtt Val | cag Gln | gat Asp 90 | ctt Leu | gaa Glu | agt Ser | aag Lys | ggc Gly 95 | ata Ile | aaa Lys | aag Lys | 346 |
| tta Leu | ato Ile | gga Gly | | gtg Val | cag Gln | atg Met 105 | FLO | gtg Val | g gca . Ala | gct Ala | gta Val 110 | gtt Val | gtt Val | atg Met | gct Ala | 394 |
| tgo Cys | s Se | cgt r Arg | act g Thi | t gad r Asp | tac Ty: | с теп | gag Glu | ago Aro | g act g Thi | att 11e 125 | | tcc Ser | ato Ile | tta Leu | aaa Lys 130 | 442 |

| tac caa aca t Tyr Gln Thr S | ct gtt go er Val Al 135 | ca tca a La Ser I | aaa tat Lys Tyl | t cct or r Pro 1 140 | ctt ttc Leu Phe | ata to Ile Se | cc cag er Gln 145 | gat Asp | 490 |
|---|-------------------------------|---------------------------|-------------------------|----------------------------|---------------------------|---------------------------|---------------------------|------------------------|------|
| gga tca aat o Gly Ser Asn I | ct gat g Pro Asp V | ta aga a al Arg l | aag ct Lys Le 15 | u Ala | ttg ago Leu Ser | tat gg Tyr GJ 10 | - <u>1</u> | ctg Leu | 538 |
| acg tat atg of Thr Tyr Met of 165 | cag cac t Gln His L | eu Asp | tat ga Tyr Gl 170 | a cct u Pro | gtg cat Val His | act gas Thr Gi 175 | aa aga lu Arg | cca Pro | 586 |
| ggg gaa ctg Gly Glu Leu 180 | gtt gca t Val Ala T | ac tac yr Tyr 185 | aag at Lys Il | t gca e Ala | cgt cat Arg Hi: | | ag tgg ys Trp | gca Ala | 634 |
| ttg gat cag Leu Asp Gln 195 | Leu Phe H | ac aag is Lys | cat aa His As | at ttt sn Phe | agc cg Ser Ar 205 | t gtt a g Val I | tc ata le Ile | cta Leu 210 | 682 |
| gaa gat gat Glu Asp Asp | atg gaa a Met Glu 1 215 | att gct [le Ala | gct ga Ala As | at ttt sp Phe 220 | ttt ga Phe As | c tat t p Tyr F | tt gag he Glu 225 | gct Ala | 730 |
| gga gct act Gly Ala Thr | ctt ctt c Leu Leu 2 | gac aga Asp Arg | ASD T | ag tcg ys Ser 35 | att at Ile Me | | att tct [le Sei 240 | tct Ser | 778 |
| tgg aat gac Trp Asn Asp 245 | aat gga Asn Gly | caa agg Gln Arg | cag t Gln P 250 | tc gtc he Val | caa ga Gln As | at cct of pro 1 255 | gat gc Asp Al | t ctt a Leu | 826 |
| tac cgc tca Tyr Arg Ser 260 | gac ttt Asp Phe | ttt cct Phe Pro 265 | GIA T | tt gga Leu Gly | , 115 11 | tg ctt et Leu 70 | tca aa Ser Ly | a tca s Ser | 874 |
| act tgg tcc Thr Trp Ser 275 | gaa cta Glu Leu | tct cca Ser Pro | aag t Lys T | gg cca Trp Pro | a aag g b Lys A 285 | ct tac la Tyr | tgg ga Trp As | t gac p Asp 290 | 922 |
| tgg cta agg | ctg aaa Leu Lys 295 | gaa aat Glu Asr | cac a | aga ggt Arg Gly 30 | y 9 - | aa ttt In Phe | att co Ile Ar 30 | gc cca cg Pro)5 | 970 |
| gaa gtt tgo Glu Val Cys | aga acg Arg Thr | tac aat Tyr Asi | i Pile | ggt ga Gly Gl 315 | g cat g u His G | ggt tct Gly Ser | agt tt Ser Le 320 | g ggg au Gly | 1018 |
| cag ttt tt Gln Phe Pho 32 | aag cag Lys Gln | tat ct Tyr Le | t gag u Glu 330 | cca at Pro Il | t aag (e Lys 1 | cta aat Leu Asn 335 | gat g Asp V | tc cag al Gln | 1066 |
| gtt gat tg Val Asp Tr 340 | | atg ga Met As 34 | р пец | agt ta Ser Ty | | ttg gag Leu Glu 350 | gac a Asp A | ac tat sn Tyr | 1114 |

| gct gat gct gtt ttg aaa gca ttt aac ata gat ggt gat gtg cgt att Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg Ile 375 cag tac aga gac caa cta gac ttt gaa gat atc gct cga cag ttt ggc Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe Gly 390 395 1210 1210 1258 | | | | | | | | | | | | |
|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Cag tac aga gac caa cta gac ttt gad gat atc get egd edg edg gar Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe Gly 390 395 | | | | | | | | | | | | |
| the and got got got gog gog gog gog tat aaa ggg 1306 | | | | | | | | | | | | |
| att ttt gaa gaa tgg aag gat ggt gta cca cgg gca gca tat aaa ggg 1306 Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys Gly 405 410 415 | | | | | | | | | | | | |
| ata gta gtt ttc cgg ttt caa aca tct aga cgt gtg ttc ctt gtt tcc 1354 Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val Ser 420 425 430 | | | | | | | | | | | | |
| cct gat tct ctt cga caa ctt gga gtt gaa gat act tag cgaagatatg 1403 Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr * 435 440 445 | | | | | | | | | | | | |
| attggagcct gagcaacaat ttagacttat ttggtaggat acatttgaaa gagctgacac 1463 gaaaagtatg actaccagta gctacatgca acattttaat gttaatggaa ggaacccact 1523 gcttattgtt ggaatggatg aatcatcacc acatcctatt attcaagttt acaaacataa 1583 agaggaaatg ttgccctata aaaacaaatt ttttgttct aagaaggaac gttacgatta 1643 tgagcaactt tggcggccgc gaattc <210> 2 <211> 446 <212> PRT <213> Solanum tuberosum | | | | | | | | | | | | |
| <400> 2 Met Arg Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val 10 15 | | | | | | | | | | | | |
| Ala Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln | | | | | | | | | | | | |
| Ser Glu Tyr Val Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His | | | | | | | | | | | | |
| Cys Thr Ser Gln Thr Arg Leu Ile Asp Lys Ile Ser Gln Gln Gln | | | | | | | | | | | | |
| 50 Gly Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu 75 80 | | | | | | | | | | | | |
| 65 /U Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile 95 | | | | | | | | | | | | |
| Lys Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val | | | | | | | | | | | | |
| 100 Met Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile | | | | | | | | | | | | |
| 115 120 Leu Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser | | | | | | | | | | | | |
| 130 135 Gln Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly 160 | | | | | | | | | | | | |
| 145 150 153 Gln Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu | | | | | | | | | | | | |

```
175
                                    170
                165
Arg Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
                                                   1.90
                                185
            180
Trp Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile
                                                 205
                            200
        195
Ile Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe
                        215
Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
                                         235
                     230
Ser Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp
                                                         255
                                     250
                245
Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
                                                     270
                                 265
            260
Lys Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
                                                 285
                             280
        275
Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile
                                             300
                         295
Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser
                                         315
                     310
Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp
                                                         335
                                     330
                 325
Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp
                                                     350
                                 345
             340
Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile
                                                 365
                             360
 His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val
                                              380
                         375
 Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln
     370
                                          395
                     390
 Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr
                                                          415
                                      410
                 405
 Lys Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu
                                                      430
                                  425
             420
 Val Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr
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 <211> 1737
 <212> DNA
  <213> Nicotiana tabacum
  <220>
  <221> misc_feature
  <222> (733)...(741)
  <223> function: Asn codon in this context is a potential
        glycosylation site;
        product: N-glycosylation consensus sequence;
        phenotype: N-glycans modulate protein properties;
        standard_name: N-glycosylation site;
        label: pot-CHO;
        note: GnTI sequences from animals do not contain
        this feature.
```

<221> CDS

<222> (127)...(1467)

```
<223> codon start: 127;
      function: initiates complex N-glycans on secretory
      glycoproteins;
      EC number: 2.4.1.101;
      product: beta-1,2-N-acetylglucosaminlytransferase I;
      evidence: EXPERIMENTAL;
      gene: cgl;
      standard name: gntI;
      label: ORF;
      note: first gntI sequence from tobacco
      (unpublished).
<221> 5'UTR
<222> (15)...(126)
<221> 3'UTR
<222> (1468)...(1723)
<221> CDS
<222> (154)...(213)
<223> function: membrane anchor (amino acids 10-29);
       product: hydrophobic amino acid stretch in GnTI;
       standard_name: membrane anchor of a type II golgi
       protein.
 <221> misc_feature
 <222> (1)...(14)
 <223> function: use for cloning the cDNA library in
       Lambda ZAPII;
       product: EcoRI/NotI-cDNA adapter;
       number: 1.
 <221> misc feature
 \langle 222 \rangle (172\overline{4})...(1737)
 <223> product: EcoRI/NotI-cDNA adapter;
       number: 2.
 gaattcgcgg ccgccattga cttgatccta actgaacagg caaagtaaat ccagcgatga 60
 aacactcata actgaacact gagagactat tcgctttctc ctaaagcctt caatcgaatt 120
 cgcacg atg aga ggg aac aag ttt tgc tgt gat ttc cgg tac ctc ctc
         Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu
  atc ttg gct gct gcc ttc atc tac aca cag atg cgg ctt ttt gcg
                                                                      216
  Ile Leu Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala
                        20
   15
  aca cag tca gaa tat gca gat cgc ctt gct gct gca att gaa gca gaa
                                                                      264
  Thr Gln Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu
                    35
  aat cat tgt aca agc cag acc aga ttg ctt att gac cag att agc ctg
                                                                      312
  Asn His Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu
                50
  cag caa gga aga ata gtt gct ctt gaa gaa caa atg aag cgt cag gac
                                                                       360
```

| Gln Gl | | ly <i>1</i> 65 | Arg | Ile | Val | Ala | Leu 70 | Gl | u G | lu (| Gln | Met | Ly 7 | s A: 5 | rg (| Gln | As | р | |
|------------------------|-------------------|-------------------|-------------------|-------------------|-----------------------|------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|---------------------|---------------------------|-------------------|-------------------|----------------|-------------------|------|
| cag ga Gln Gl | | | cga Arg | caa Gln | tta Leu | agg Arg 85 | gct Ala | ct Le | t g u V | tt al | cag Gln | gat Asp 90 | | t g u G | aa (| agt Ser | aa Ly | g 's | 408 |
| ggc at Gly II 95 | ta a le I | aa .ys | aag Lys | ttg Leu | atc Ile 100 | gga Gly | aat Asn | gt Va | a c | ag Sln | atg Met 105 | cca Pro | gt Va | g g l A | ct | gct Ala | gt Vā 11 | _ | 456 |
| gtt g Val V | tt a al N | atg Met | gct Ala | tgc Cys 115 | aat Asn | cgg Arg | gct Alá | ga As | şħ. | ac Tyr 120 | ctg Leu | gaa Glu | ı aa | ıg a 7s T | nct Thr | att Ile 125 | aa Ly | aa ys | 504 |
| tcc a Ser I | tc t le 1 | tta Leu | aaa Lys 130 | tac Tyr | caa Gln | ata Ile | tci Se: | r v | tt d al 2 35 | gcg Ala | tca Ser | aaa Lys | a ta | , | cct Pro 140 | ctt Leu | t Pl | tc he | 552 |
| ata t Ile S | er (| cag Gln 145 | gat Asp | gga Gly | tca Ser | cat | cc Pr 15 | O A | at sp | gtc Val | agg Arg | aa Ly | ٠ ـــ | tt d eu <i>l</i> 55 | gct Ala | ttg Leu | a S | gc er | 600 |
| tat q Tyr <i>F</i> | gat Asp 160 | cag Gln | ctg Leu | acg Thr | tat Tyr | ato Met 16 | r Gr | g c n H | ac | ttg Leu | gat Asp | tt Ph 17 | | aa lu | cct Pro | gtg Val | ј С | at is | 648 |
| act (Thr (| gaa Glu | aga Arg | cca Pro | ggg Gl | g gaq 7 Glu 180 | і Ге | g at u Il | t g .e <i>P</i> | jca Ala | tac Tyr | ta Ty: 18 | <u>, ,, ,</u> | a a s I | tt le | gca Ala | cgt Arg | , | at Iis .90 | 696 |
| tac Tyr | aag Lys | tgg Trp | gca Ala | tto Lev 19 | ı Ası | t ca p Gl | g ct n Le | eu I | tt Phe | tac Tyr 200 | . பу | g ca s Hi | it a .s P | at Asn | ttt Phe | age Se: 20 | | gt Arg | 744 |
| gtt Val | atc Ile | ata Ile | cta Lei 210 | ı Gl | a ga u As | t ga p As | t at | 9T (| gaa Glu 215 | att Ile | gc Al | c co a Pi | ct q co <i>l</i> | gat Asp | ttt Phe 220 | | t d e i | gac Asp | 792 |
| ttt Phe | ttt Phe | gaç Glu 225 | ı Al | t gg a Gl | a gc y Al | a irr | r L | eu | ьeu | no | O LIT | ja ga gg A | JP . | -,~ | tco Sei | g at r Il | t e | atg Met | 840 |
| gct Ala | att Ile 240 | tc: Se: | | t tg r Tr | g aa p As | in As | ac a sp A 45 | at sn | gga Gly | ca Gl | a at n Me | | ag ln 50 | ttt Phe | gt Va | c ca l Gl | a .n | gat Asp | 888 |
| cct Pro 255 | | | t ct a Le | t ta u Ty | ac co yr Ai 20 | gc to cg So | ca g er A | at | ttt Phe | tt Ph | C 1. | cc g ro G 65 | gt ly | ctt Leu | gg Gl | a to y Ti | p gg | atg Met 270 | 936 |
| | tca Ser | a aa C Ly | a to 's Se | er Ti | ct to nr T: 75 | gg g rp A | ac g sp (| gaa Slu | tta Lei | a to 1 Se 28 | : L | ca a ro I | ag ys | tgg Trp | g cc Pr | | ag ys 85 | gct Ala | 984 |
| tac Tyr | tg: | g ga o As | ic ga | ac t sp T | gg c rp L | ta a eu A | ga (.rg] | ctc Leu | aaa Ly: | a ga s Gl | aga Lu A | at d sn 1 | cac His | aga Arg | a go g Gl | gt c | ga rg | caa Gln | 1032 |

| 290 |) | 295 | 300 | | | | | | | |
|--|---|--|--|--|--|--|--|--|--|--|
| ttt att cgc cca Phe Ile Arg Pro 305 | a gaa gtt tgc aga o Glu Val Cys Arg 310 | aca tat aat ttt ggt Thr Tyr Asn Phe Gly 315 | gag cat ggt 1080 Glu His Gly | | | | | | | |
| tct agt ttg ggg Ser Ser Leu Gly 320 | g cag ttt ttc aag y Gln Phe Phe Lys 325 | cag tat ctt gag cca Gln Tyr Leu Glu Pro 330 | att aaa cta 1128 Ile Lys Leu | | | | | | | |
| aat gat gtc ca Asn Asp Val Gl 335 | g gtt gat tgg aag n Val Asp Trp Lys 340 | tca atg gac ctt agt Ser Met Asp Leu Ser 345 | tac ctt ttg 1176 Tyr Leu Leu 350 | | | | | | | |
| gag gac aat ta Glu Asp Asn Ty | c gtg aaa cac ttt r Val Lys His Phe 355 | ggt gac ttg gtt aaa Gly Asp Leu Val Lys 360 | aag gct aag 1224 Lys Ala Lys 365 | | | | | | | |
| ccc atc cat gg Pro Ile His Gl 37 | y Ala Asp Ala vai | ttg aaa gca ttt aac Leu Lys Ala Phe Asn 375 | ata gat ggt 1272 Ile Asp Gly 380 | | | | | | | |
| gat gtg cgt at Asp Val Arg Il 385 | ct cag tac aga gat Le Gln Tyr Arg Asg 390 | caa cta gac ttt gaa o Gln Leu Asp Phe Glu) 395 | 11011 === | | | | | | | |
| cgg caa ttt gg Arg Gln Phe Gl 400 | gc att ttt gaa gaa ly Ile Phe Glu Glu 405 | a tgg aag gat ggt gta u Trp Lys Asp Gly Val 410 | a cca cgt gca 1368 L Pro Arg Ala | | | | | | | |
| gca tat aaa go Ala Tyr Lys G 415 | ga ata gta gtt tto ly Ile Val Val Ph 420 | c cgg tac caa acg tco e Arg Tyr Gln Thr Sei 425 | c aga cgt gta 1416 r Arg Arg Val 430 | | | | | | | |
| ttc ctt gtt g Phe Leu Val G | gc cat gat tcg ct ly His Asp Ser Le 435 | t caa caa ctc gga at u Gln Gln Leu Gly Il 440 | t gaa gat act 1464 e Glu Asp Thr 445 | | | | | | | |
| taa caaagatat * | g attgcaggag cccg | ggcaaa atttttgact ta | ttgggtag 1517 | | | | | | | |
| gatgcatcga gctgacacta aaccatgatt ttaccagtta catacaacgt tttaatgtta 1577 tacggaggag ctcactgttc tagtgttgaa gggatatcgg cttcttagta ttggatgaat 1637 catcaacaca acctattatt ttaagtgttc agaacataaa gaggaaatgt agccctgtaa 1697 agactataca tgggaccatc ataatcgcgg ccgcgaattc | | | | | | | | | | |
| <210> 4 <211> 446 <212> PRT <213> Nicotia | ana tabacum | | | | | | | | | |
| | | ys Asp Phe Arg Tyr Le 10 hr Gln Met Arg Leu Pl 25 | | | | | | | | |

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Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His
                           40
Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu Gln Gln
Gly Arg Ile Val Ala Leu Glu Glu Gln Met Lys Arg Gln Asp Gln Glu
                   70
Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
                                   90
                85
Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val Val
                               105
           100
Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys Ser Ile
                           120
Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
                       135
Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Asp
                                      155
                   150
Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His Thr Glu
                                                      175
                                  170
               165
Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
                               185
           180
Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Asn Phe Ser Arg Val Ile
                                    205
                           200
 Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Phe Phe
                                          220
                        215
 Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
                                      235
                    230
 Ser Ser Trp Asn Asp Asn Gly Gln Met Gln Phe Val Gln Asp Pro Tyr
                                   250
                245
 Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
                                                  270
                                265
            260
 Lys Ser Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
                            280
 Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile
                                           300
                        295
 Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser
                                       315
                     310
 Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp
                                   330
                 325
 Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp
                                                    350
                                345
 Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile
                            360
 His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val
                                            380
                         375
 Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asn Ile Ala Arg Gln
                                       395
                     390
  Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr
                                    410 415
                 405
  Lys Gly Ile Val Val Phe Arg Tyr Gln Thr Ser Arg Arg Val Phe Leu
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```

<212> DNA

<213> Arabidopsis thaliana

```
<220>
<221> misc feature
<222> (1185)...(1193)
<223> function: Asn Codon is a potential glycosylation
      product: Consensus sequence for N-glycosylation;
      phenotype: N glycans modulate protein
      characteristics;
      standard name: N glycosylation site;
      label: pot-CHO;
      note: absent in animal GnTI sequences.
<221> CDS
<222> (135)...(1469)
<223> codon start: 135;
      function: initiates complex N glycans on secretory
       glycoproteins;
       EC number: 2.4.1.101;
      product: beta-1,2-N-acetyl glucosaminyl
       transferase I;
       evidence: EXPERIMENTAL;
       gene: cgl;
       standard name: gntI;
       label: ORF;
       note: first gntI sequence from Arabidopsis
       (unpublished).
 <221> 5'UTR
 <222> (19)...(134)
 <221> 3'UTR
 <222> (1470)...(1848)
 <221> CDS
 <222> (157)...(215)
 <223> function: membrane anchor (amino acids 8-27);
       product: hydrophobic amino-acid region in GnTI;
       standard_name: membrane anchor of a Type II Golgi
        protein;
        note: identified by comparison with animal GnTI
        sequences.
  <221> misc feature
  <222> (1)...(18)
  <223> function: for preparation of a cDNA library in
        Lambda ACT;
        product: XhoI-cDNA-Adaptor;
        number: 1.
  <221> misc feature
  \langle 222 \rangle (184\overline{9}) \dots (1854)
  <223> product: XhoI-cDNA-Adaptor;
        number: 2.
  ctcgaggcca cgaaggccac cgtttttgtt ataacgaacg acaccgtttc aaacaacttc 60
  <400> 5
  cttattagct agctccctcc cggcggcaaa caccagaaga tccaccgctt ttgatctggt 120
```

| tgtttgtcgt cgat | atg gcg Met Ala 1 | agg atc Arg Ile | tcg Ser | tgt (Cys <i>l</i> | gac t Asp I | tg a Leu <i>l</i> | aga t Arg I | ttt Phe 10 | ctt Leu | ctc Leu | 170 |
|--|-------------------------------|-----------------------------|-----------------------|-----------------------|-----------------------|----------------------|----------------------|-------------------|-------------------|-----------------------|-----|
| atc ccg gca gct Ile Pro Ala Ala 15 | ttc atg Phe Met | ttc atc Phe Ile 20 | tac Tyr | atc (Ile (| cag a Gln N | atg a Met i | agg o Arg 1 25 | ctt Leu | ttc Phe | cag Gln | 218 |
| acg caa tca cag Thr Gln Ser Gln 30 | tat gca Tyr Ala | gat cgc Asp Arg 35 | ctc Leu | agt Ser | tcc (Ser <i>l</i> | gct Ala 40 | atc (| gaa Glu | tct Ser | gag Glu | 266 |
| aac cat tgc act Asn His Cys Thr 45 | agt caa Ser Gln 50 | atg cga Met Arg | ggc | ctc Leu | ata (Ile) 55 | gat Asp | gaa Glu | gtt Val | agc Ser | atc Ile 60 | 314 |
| aaa cag tcg cgg Lys Gln Ser Arg | att gtt Ile Val 65 | gcc ctc Ala Leu | gaa Glu | gat Asp 70 | atg Met | aag Lys | aac Asn | cgc Arg | cag Gln 75 | gac Asp | 362 |
| gaa gaa ctt gtg Glu Glu Leu Val 80 | Gln Leu | aag gat Lys Asp | cta Leu 85 | atc Ile | cag Gln | acg Thr | ttt Phe | gaa Glu 90 | aaa Lys | aaa Lys | 410 |
| gga ata gca aaa Gly Ile Ala Lys 95 | a ctc act s Leu Thr | caa ggt Gln Gly 100 | Y GIY | cag Gln | atg Met | cct Pro | gtg Val 105 | gct Ala | gct Ala | gta Val | 458 |
| gtg gtt atg gc Val Val Met Ala 110 | c tgc agt a Cys Ser | cgt gca Arg Ala 115 | a gac a Asp | tat Tyr | ctt Leu | gaa Glu 120 | agg Arg | act Thr | gtt Val | aaa Lys | 506 |
| tca gtt tta ac Ser Val Leu Th 125 | a tat caa r Tyr Gln 130 | Thr Pr | c gtt o Val | gct Ala | tca Ser 135 | aaa Lys | tat Tyr | cct Pro | cta | ttt Phe 140 | 554 |
| ata tct cag ga Ile Ser Gln As | t gga tct p Gly Ser 145 | gat ca Asp Gl | a gct n Ala | gtc Val 150 | гда | agc Ser | aag Lys | tca Ser | tto Lei 155 | JUCI | 602 |
| tat aat caa tt Tyr Asn Gln Le 16 | u Thr Tyi | atg ca Met Gl | g cac n His 165 | Leu | gat Asp | ttt Phe | gaa Glu | cca Pro 170 | va. | g gtc l Val | 650 |
| act gaa agg co Thr Glu Arg Pr 175 | t ggt gaa o Gly Gli | a ctg ac ı Leu Th 18 | ir Ala | g tac Tyr | tac Tyr | aag Lys | att Ile 185 | HIC | a Cg | t cac g His | 698 |
| tac aag tgg go Tyr Lys Trp Al 190 | a ctg ga a Leu As | c cag tt p Gln Le 195 | ig ttt eu Phe | tac Tyr | aaa Lys | cac His | у пуз | ttt Phe | ag e Se | t cga r Arg | 746 |
| gtg att ata ct Val Ile Ile Le 205 | a gaa ga eu Glu As 21 | p Asp Me | ig gaa et Glu | a att u Ile | gct Ala 215 | LIC | a gad o Asp | c tto Pho | c tt e Ph | t gat e Asp 220 | 794 |
| tac ttt gag g | ct gca gc | t agt c | tc at | g gat | t agg | g gat | t aaa | a ac | c at | t atg | 842 |

| Tyr | Phe | Glu | Ala | Ala 225 | Ala | Ser | Leu | Met | Asp 230 | Arg | Asp | Lys | Thr | Ile 235 | Met | |
|-------------------|-----------------------|-------------------|-----------------------|---------------------|-------------------|-------------------|-----------------------|-----------------------|-------------------|-------------------|-------------------|-----------------------|---------------------|-------------------|-------------------|------|
| gct Ala | gct Ala | tca Ser | tca Ser 240 | tgg Trp | aat Asn | gat Asp | aat Asn | gga Gly 245 | cag Gln | aag Lys | cag Gln | ttt Phe | gtg Val 250 | cat His | gat Asp | 890 |
| ccc Pro | tat Tyr | gcg Ala 255 | cta Leu | tac Tyr | cga Arg | tca Ser | gat Asp 260 | ttt Phe | ttt Phe | cct Pro | ggc Gly | ctt Leu 265 | ggg | tgg Trp | atg Met | 938 |
| ctc Leu | aag Lys 270 | aga Arg | tcg Ser | act Thr | tgg Trp | gat Asp 275 | gag Glu | tta Leu | tca Ser | cca Pro | aag Lys 280 | tgg Trp | cca Pro | aag Lys | gct Ala | 986 |
| tac Tyr 285 | tgg Trp | gat Asp | gat Asp | tgg Trp | ctg Leu 290 | aga Arg | cta Leu | aag Lys | gaa Glu | aac Asn 295 | cat His | aaa Lys | ggc Gly | cgc Arg | caa Gln 300 | 1034 |
| ttc Phe | att Ile | gca Ala | ccg Pro | gaa Glu 305 | gtc Val | tgt Cys | aga Arg | aca Thr | tac Tyr 310 | aat Asn | ttt Phe | ggt Gly | gaa Glu | cat His 315 | Gly ggg | 1082 |
| tct Ser | agt Ser | ttg Leu | gga Gly 320 | cag Gln | ttt Phe | ttc Phe | agt Ser | cag Gln 325 | tat Tyr | ctg Leu | gaa Glu | cct Pro | ata Ile 330 | aag Lys | cta Leu | 1130 |
| aac Asn | gat Asp | gtg Val 335 | Thr | gtt Val | gac Asp | tgg Trp | aaa Lys 340 | Ala | aag Lys | gac Asp | ctg Leu | gga Gly 345 | tac Tyr | ctg Leu | aca Thr | 1178 |
| gag Glu | gga Gly 350 | Asn | tat Tyr | acc Thr | aag Lys | tac Tyr 355 | Phe | tct Ser | ggc | tta Leu | gtg Val 360 | . Arg | caa Gln | gca Ala | cga Arg | 1226 |
| cca Pro 365 | Ile | caa Gln | ggt Gly | tct Ser | gac Asp 370 | Leu | gtc Val | : tta Leu | aac Lys | gct Ala 375 | GIT | aac Asn | ata Ile | aag Lys | gat Asp 380 | 1274 |
| gat Asp | gat Asp | cgt Arg | , Ile | c cgg Arg 385 | ı Tyr | Lys | : Asp | o Glr | . Val | . Glu | j ttt i Ph∈ | gaa Glu | cgc Arg | att Ile 395 | gca Ala | 1322 |
| ggç Gly | g gaa / Glu | ttt Phe | z ggt e Gly 400 | / Ile | a ttt e Phe | gaa Glu | a gaa ı Glu | a tgg ı Trp 405 | ь Гуз | g gat s Asp | ggt Gly | t gto y Val | g cca Pro 410 | Arc | a aca g Thr | 1370 |
| gca Ala | a tat a Tyi | aaa Lys 41 | s Gl | a gta y Val | a gto l Val | g gto L Val | g tt! l Phe 420 | e Arg | a ato | c caq e Glr | g aca | a aca r Thi 425 | HIG | a cgt g Arg | g ta g Val | 1418 |
| tto Phe | c cto e Leo 430 | ע Va. | t gg 1 Gl | g cca y Pro | a gat o Asj | t tc Se: | r Va. | a atq l Me | g ca t Gl: | g cti n Lei | t gga u Gl: | Х тт€ | t cga e Arq | a aat g Ası | t tcc n Ser | 1466 |
| tg: | a tg | caaa | acat | atg | aaag | gaa | aaga | agat | tt t | ggac | cgca | t gc | agcc | tcct | | 1519 |

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tctagcagct gttaggttgt attgttattt atggatgagt ttgtagagcg gtggggttaa 1579
ctttaacagc aaggaagete tggtgaccag getgattgge ttagaagtta tgggaaccec 1639
ttgaaagggt cagggttaaa tatatttcag ttgttttatt agtgattatc ttgtgggtaa 1699
cttatacgaa tgcaaatcat tctatgcagt ttttcttcgt cccacttgtt ttggcttctc 1759
tattgctagt gtacatatct cttcaaacat gtactaaata atgcgtgttg cttcaaagaa 1819
gtaactttta ttaaaaaaaa aaaaaaaaac tcgag
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<211> 444
<212> PRT
<400> 6
Met Ala Arg Ile Ser Cys Asp Leu Arg Phe Leu Leu Ile Pro Ala Ala
                                      10
Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln Thr Gln Ser Gln
                                                      30
                                  25
             20
Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu Asn His Cys Thr
                              40
         35
Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile Lys Gln Ser Arg
Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp Glu Glu Leu Val
                                          75
                      70
Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys Gly Ile Ala Lys
                                      90
                  85
Leu Thr Gln Gly Gln Met Pro Val Ala Ala Val Val Met Ala
                                 105
             100
 Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys Ser Val Leu Thr
                             120
         115
 Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp
                                              140
                         135
 Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser Tyr Asn Gln Leu
                                          155
                     150
 Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val Val Thr Glu Arg Pro
                                                          175
                                      170
                 165
 Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala
                                                      190
                                  185
             180
 Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg Val Ile Ile Leu
                              200
 Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Tyr Phe Glu Ala
                                              220
                          215
 Ala Ala Ser Leu Met Asp Arg Asp Lys Thr Ile Met Ala Ala Ser Ser
                                          235
                      230
 Trp Asn Asp Asn Gly Gln Lys Gln Phe Val His Asp Pro Tyr Ala Leu
                                                          255
                                      250
                  245
 Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Lys Arg Ser
                                                      270
                                  265
              260
 Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp
                                                  285
                              280
          275
  Trp Leu Arg Leu Lys Glu Asn His Lys Gly Arg Gln Phe Ile Ala Pro
                                               300
                          295
  Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu Gly
                                                               320
                                           315
                      310
  Gln Phe Phe Ser Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val Thr
                                                           335
                                      330
                  325
  Val Asp Trp Lys Ala Lys Asp Leu Gly Tyr Leu Thr Glu Gly Asn Tyr
                                                       350
                                   345
              340
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Thr Lys Tyr Phe Ser Gly Leu Val Arg Gln Ala Arg Pro Ile Gln Gly
                             360
       355
Ser Asp Leu Val Leu Lys Ala Gln Asn Ile Lys Asp Asp Asp Arg Ile
                         375
Arg Tyr Lys Asp Gln Val Glu Phe Glu Arg Ile Ala Gly Glu Phe Gly
                                         395
                    390
Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Thr Ala Tyr Lys Gly
                                                         415
                                     410
                405
Val Val Phe Arg Ile Gln Thr Thr Arg Arg Val Phe Leu Val Gly
                                 425
            420
Pro Asp Ser Val Met Gln Leu Gly Ile Arg Asn Ser
                             440
<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer for cloning plant genes
<221> misc_feature
 <222> (6) ... (12)
 <223> n at positions 6, 9 & 12 = inosine.
 <400> 7
                                                                     24
 tgygynwsng cntggmayga yaay
 <210> 8
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <223> Primer for cloning plant genes
 <221> misc feature
 <222> (4)...(10)
 <223> n at positions 4, 7, & 10 = inosine.
 <221> misc feature
  <222> 13
  \langle 223 \rangle n = a, c, g, or t.
  <400> 8
                                                                      24
  ccancentrn cengsraara arte
  <210> 9
  <211> 14
  <212> PRT
  <213> Artificial Sequence
  <220>
  <223> Primer for cloning plant genes
  <221> VARIANT
  <222> 2
```

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\langle 223 \rangle Xaa = Arg or Met.
<221> VARIANT
<222> 9
<223> Xaa = Asp or Tyr.
<400> 9
Gln Xaa Gln Phe Val Gln Asp Pro Xaa Ala Leu Tyr Arg Ser
                  5
<210> 10
<211> 48
<212> DNA
<213> Artificial Sequence
<223> Primer for cloning plant genes
atcggaaagc ttggatcccc agtggcrgct gtagttgtta tggcttgc
                                                                     48
<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence
<223> Primer for cloning plant genes
<400> 11
                                                                      27
ggcccccct cgaggtcgac ggtatcg
<210> 12
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer for cloning plant genes
 gggcctctag actccagage yactactctt ccttgctgct ggctaatctt g
 <210> 13
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer for cloning plant genes
 <400> 13
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 catggatccc tcgagaagcg tcaggaccag gagtgccggc
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 <211> 37
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<212> DNA <213> Artificial Sequence <220> <223> Primer for cloning plant genes <400> 14 atcccgggat ccgctacgta tcttcaactc caagttg

37